

1  
tgt ata ata aag ctt cat aat ata aaa ttt taa ATG ACC ATC ACT TAT GAT GAA CTA AAT  
M T I T Y D E L N

61  
AAT TTG ATT AGA AAT GGA AAA ATT GAC ACG GTA GTT TTG GCA TGC GTC GAC ATG CAA GGC  
N L I R N G K I D T V V L A C V D M Q G

121  
CGG CTG ATG GGC AAG AGA TTA ACT GGG CGT CAT TTT TTA GGA TTG GAT CAA AAG AAG ATT  
R L M G K R L T G R H F L G L D Q K K I

181  
AGC ATT AGC ACG TTT GTA TAT GCG GTA ACT ATA GAA GGC ATC GCT GGC GGA GGT TAT GAG  
S I S T F V Y A V T I E G I A G G G Y E

241  
ATC TCA AGT GTA GAC ACA GGT TAT AGT GAT TGT CAT CTC TGT GCA GAT TTG AAT TCC CTT  
I S S V D T G Y S D C H L C A D L N S L

301  
CAT TTA CTC CCG TGG TCA GAA GGC GCT GTA TTG GCA ATT TCC AAT CCT CAT AAT TTC GTT  
H L L P W S E G A V L A I S N P H N F V

361  
ACT TCT GAG CCA TTG TTC TGT TCT CCT CGA GTA ATA CTC ATG CAG CAA ATT GAG CGC CTG  
T S E P L F C S P R V I L M Q Q I E R L

421  
GCT AAT CTA AAG CTT AAA GGC CTT TTT GCT TCT GAA CTA GAA TTT AAT CTT TTC AAC GAA  
A N L K L K G L F A S E L E F N L F N E

481  
ACT TAT AAG AGT GCC AGC CAA AAG CAT TGG AAA AAT TTA AAA ACC GCG CAG CCT CAT CAT  
T Y K S A S Q K H W K N L K T A Q P H H

541  
CAA TGG ATG AAT ATT AGT GCA AGT AGT GGG ATT GAA ACT TTT ATG CGT TCT GTG CGT AAT  
Q W M N I S A S S G I E T F M R S V R N

601  
AAA TTA GAA GAA GCC GGT ATT TTG ATG GAG GCG ACA CAT CCC GAA TTT TTA CCT AGT CAG  
K L E E A G I L M E A T H P E F L P S Q

661  
CAT GAA CTT AAT TTT GTA CCA GCC GAT CCT CTA ACA ATG GCA GAT CGT CAT ATT ATT GCA  
H E L N F V P A D P L T M A D R H I I A

FIGURE 1A

721

AAA CAT GGA GTT CGC GAA ATG GCA GAA CAG TCT GGA ATG GTT GCA ACT TTT ATG GCT AAA  
K H G V R E M A E Q S G M V A T F M A K

781

TTG AGT TCA ACT GCG CTT GGT AAT GCC TGC CAT ATT CAT ATG TCA CTT CAA GAT GCA GAA  
L S S T A L G N A C H I H M S L Q D A E

841

ACA GAA AAA AAT GCA TTT TAT GAT CAA AAC GAT GAA TAT GGA ATG TCA ACC TTA GCT CGT  
T E K N A F Y D Q N D E Y G M S T L A R

901

AAT TGG ATT GCT GGA TTA TTG AAA TAC GTA CCT GAA GCG ACT TAT TTC TTT GCA TCT TAC  
N W I A G L L K Y V P E A T Y F F A S Y

961

ATC AAC TCG TAC AAA AGA CTT CAA CCG CTT ACT TTT GCG CCA ACA AAA TGT TGT TGG GCA  
I N S Y K R L Q P L T F A P T K C C W A

1021

ATT GAC AAC CGA ACA AGC GCC TTT CGA CTT TGT AAT TCA AAA TCC GAG GGA ATT AAT GTT  
I D N R T S A F R L C N S K S E G I N V

1081

GAG CTG CGT ATT GGT GGC GCT GAT TTG AAC CCT TAT TTA GCT TTT TCC GCA ATC ATA GCT  
E L R I G G A D L N P Y L A F S A I I A

1141

GCA GGA ATT AGC GGT ATA GAA GAA AAG CTT GAA CTT CCC CCT CCT GCA TCT GGC AAT GTT  
A G I S G I E E K L E L P P P A S G N V

1201

TAC AAT GAT AAG GAA TTA CCT GAA TTT CCT AAT TCC TTA CAA AAT GCT ACA CAT CTT CTA  
Y N D K E L P E F P N S L Q N A T H L L

1261

AAA GAA TCG AAA ATG CTG AAT AAA ACA TTC GGG GAG AAG TTG ATT CTA CAT TAT GTA AAC  
K E S K M L N K T F G E K L I L H Y V N

1321

GCT GCT AAT GTT GAG ATT AAT GAA TTT TCA AAA CAA GTT ACT GAC TGG GAG CTT AAT CAA  
A A N V E I N E F S K Q V T D W E L N Q

1381

GGA TTT AAT AGA TAT TAA tat ttt aat gct tat gta gat aac aat caa aaa tat aat ctt  
G F N R Y \*

1441

taa ata cat aat taa aaa aaa aaa aaa a

FIGURE 1B

## Amino Acid Alignment

1 *M. incognita* Glutamine Synthetase

2 *M. tuberculosis* Glutamine Synthetase

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1 MT.....ITYDELNNLIRNGKIDTVVLACVDMOGRLMGKRLTGRHELGLDQKKISIST: 53
2 MTGPGSPPLAWTELERLVAAGDVDTVIVAFDTMOGRLAGKRISGRHFVDDIATRGVECCS: 60

1 FVYAVTIEGIAGGGYEISSVDTCVSDCHLCADLNSLHLLPWSECAVLATSNPHNFVTSEP:113
2 YLLAVDVDLNTVPGYAMASWDTCVSDMVMTPDLSTLERLIPWLPGTALVLIADLVWADGSE.:119

1 LFCSPRVILMQOIERLANLKLKGLFASELEFNLENETYKSASQKHWKNLKTAPPHQWMN:173
2 VAVSPRSILRRQLDRLLKARGLVADVATELEFIVEDQPYRQAWASGYRGLTPASDYNIDYA:179

1 ISASSGIETFMRSVRNKLEEGILMEATHPEFLPSQHELNEVPADPITMADRHIIAKHGV:233
2 ILASSRMEPLLRDIRLGMAGAGLRFEAVKGECNMGQOEIGERYDEALVTCDNHATYKNGA:239

1 REMAEQSGMVATFMAKLSSTALGNACHIHMSLQDAETEKNAFYDQND EYGMSTLARNWIA:293
2 KEIADQHGKSLTFMAKYD.EREGNSCHIHVSLRGTGDS.AVFADSNGPHGMSMFRSFVA:297

1 GLLKYPPEATYFFASYINSYKRLQPLTFAPTKCCWAIDNRTSAFRLCNSKSEGTINVELRI:353
2 GOLATLREFTLCYAPTINSYKRFADSSFAPTALAWGLDNRTCALRVVG.HGQNRVECRV:356

1 GGADLNPYLAFSAITLAAGISGIEKLELBPFPASGNVYNDKELPEFENSLOQATHLLKESK:413
2 PGGDVNQYLAVAALLAGGLYGIERGLQLPEPCVGNAYQGADVERLEPVTLADAAVLFDSDA:416

1 MLNKTGGEKLILHYVNAANVEINEFSKQVTDWELNOGFNRY:454
2 LVREAFGEDVVAHYLNNARVELAAFNAAVTDWERIRGFERL:457
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FIGURE 2